





FIGURE 2A.

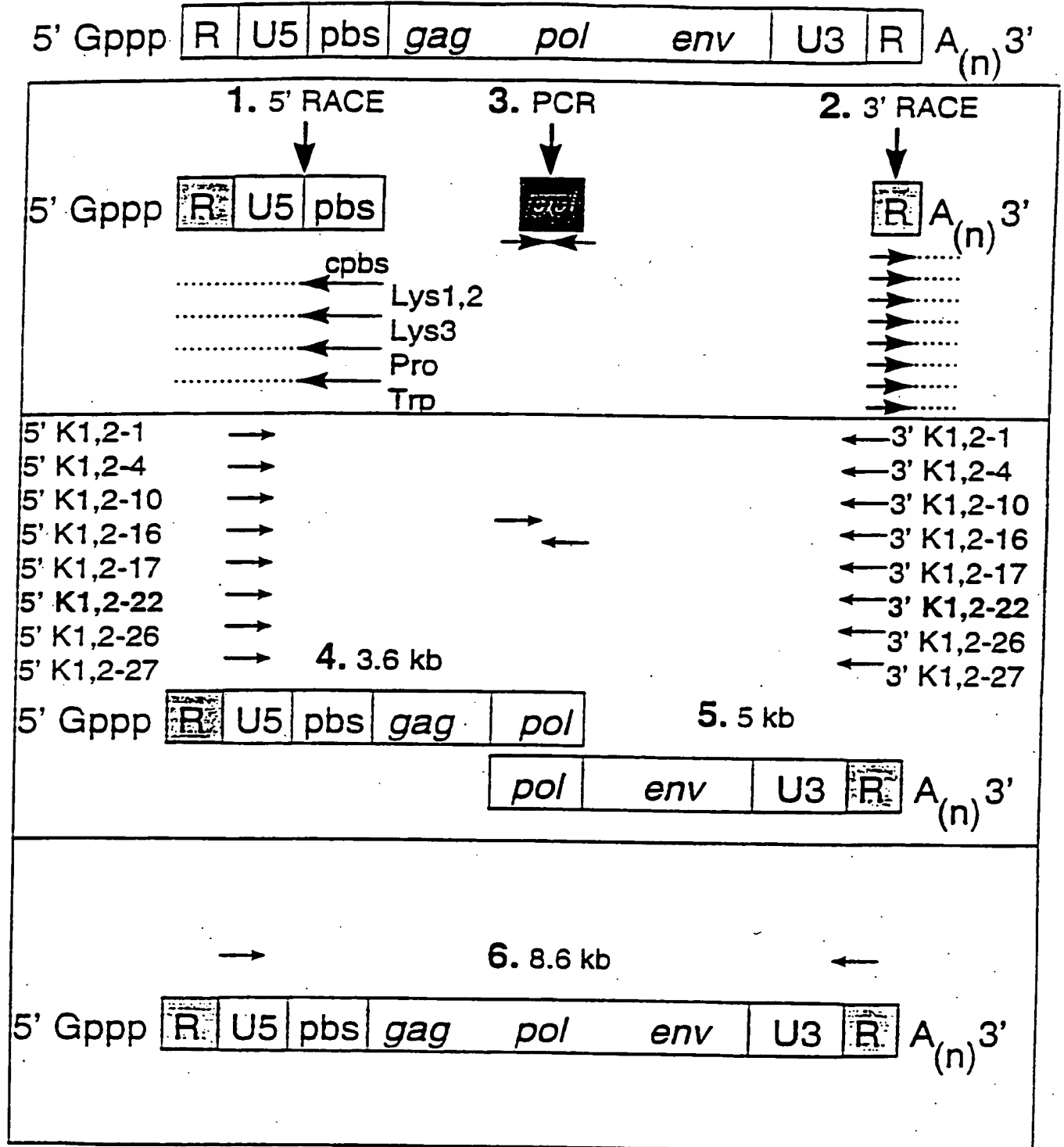
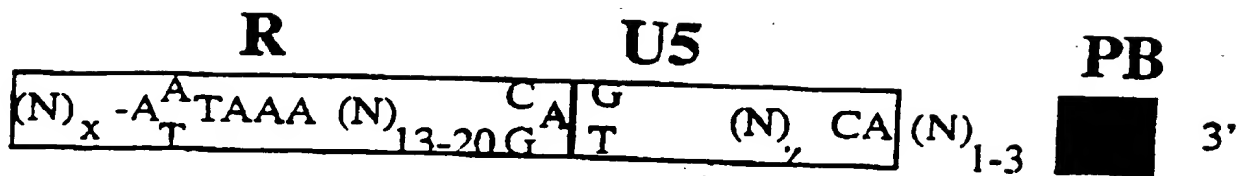


FIGURE 2B



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FIGURE 2C

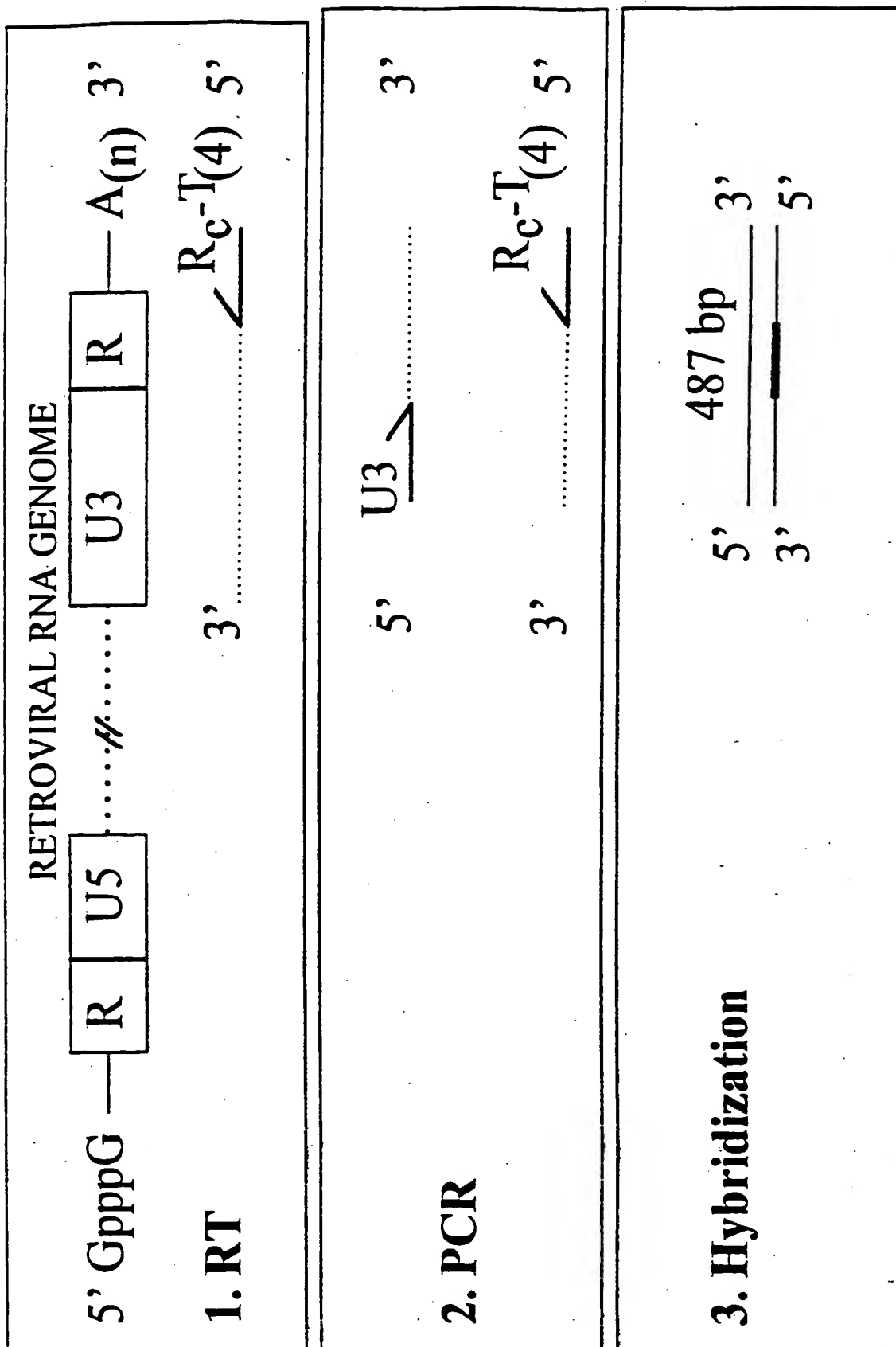


FIGURE 2D

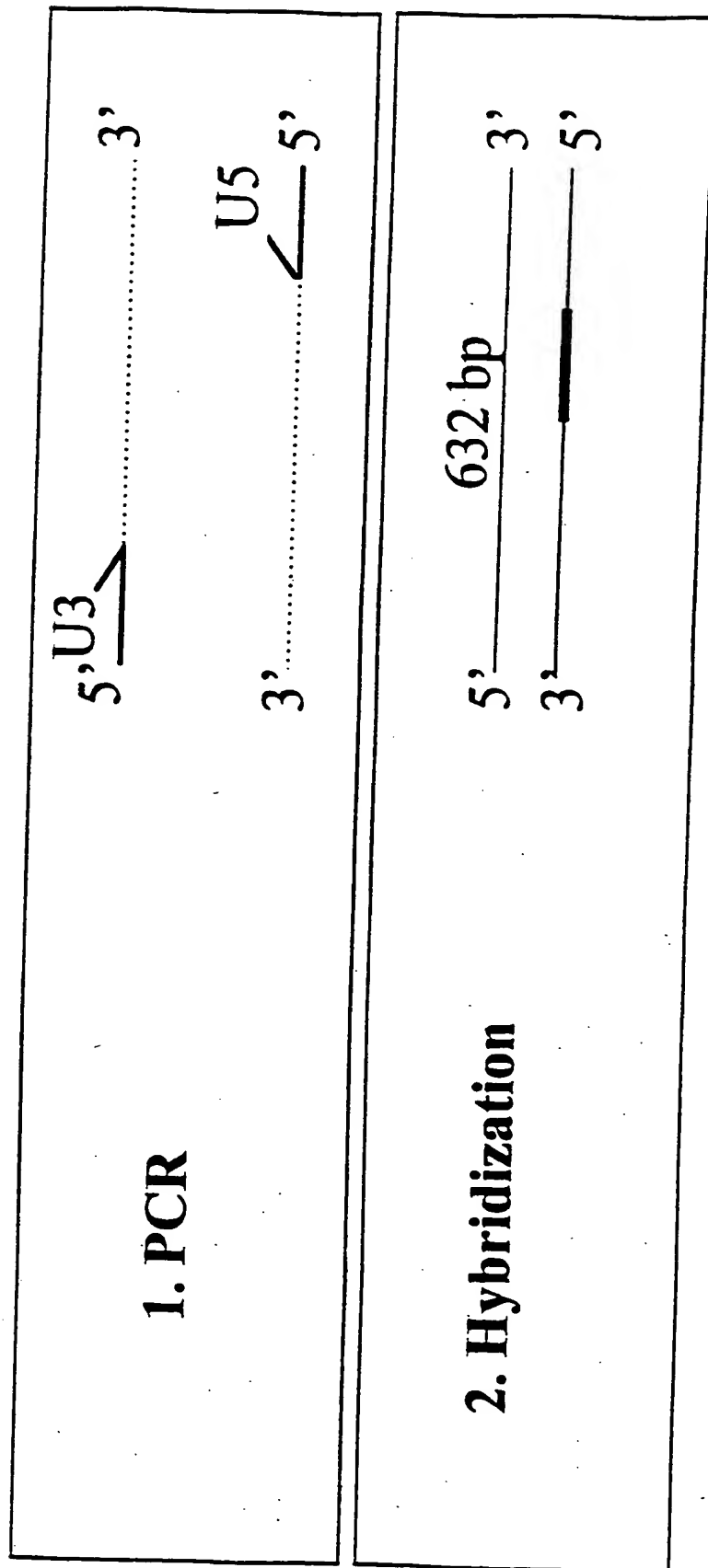
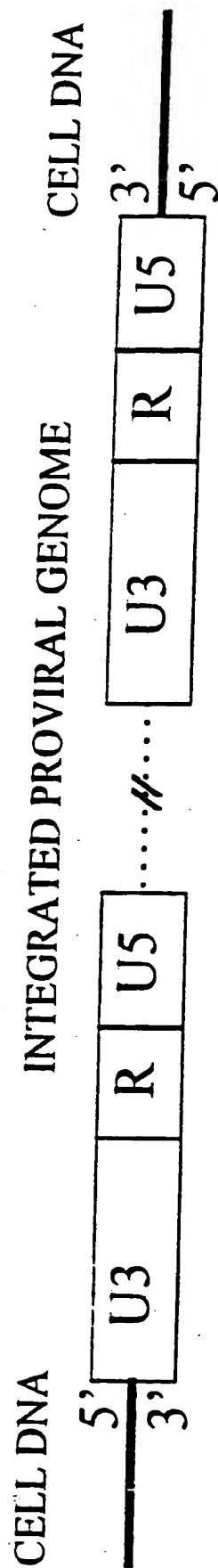


FIGURE 2E

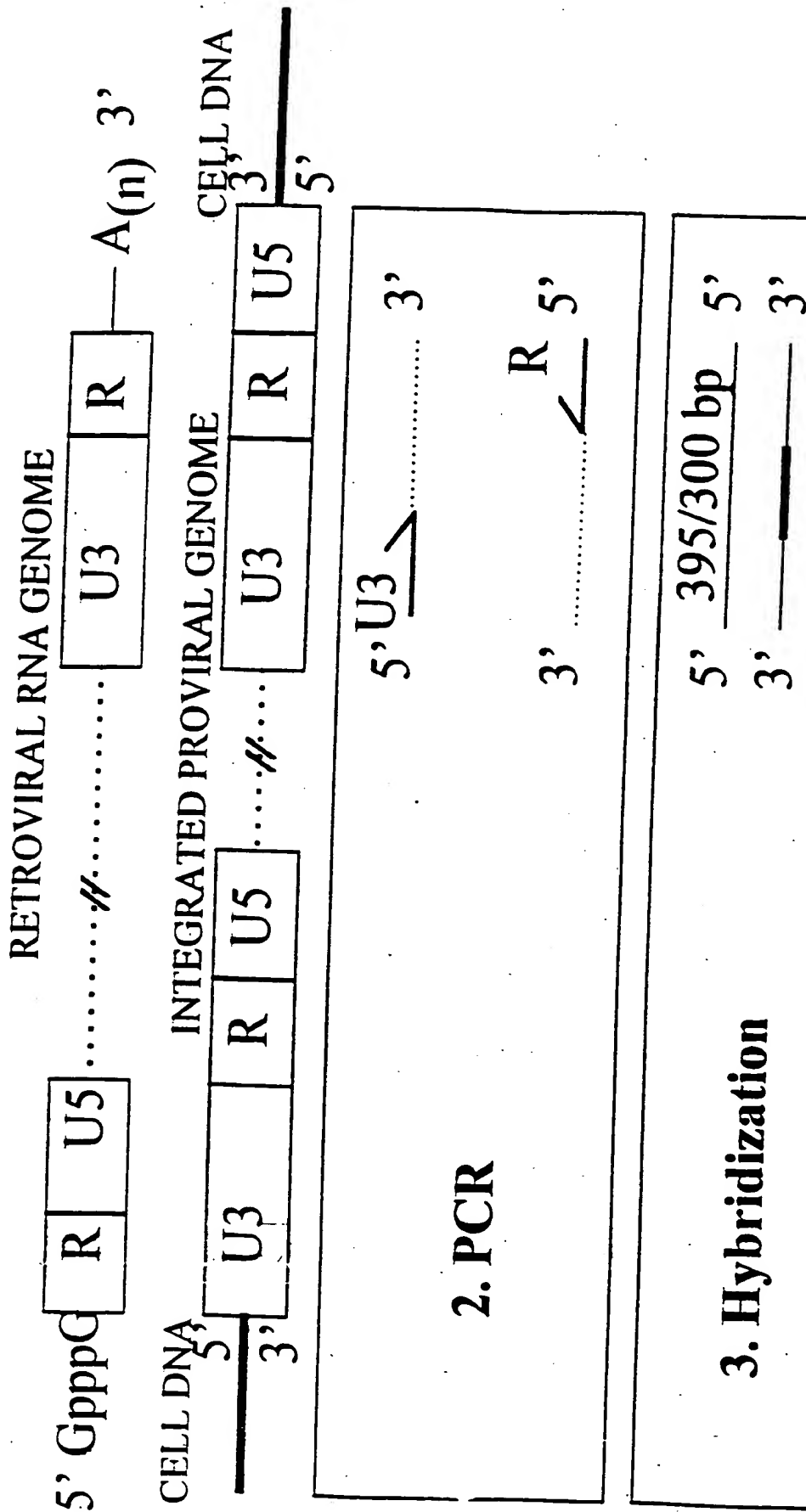


FIGURE 2F











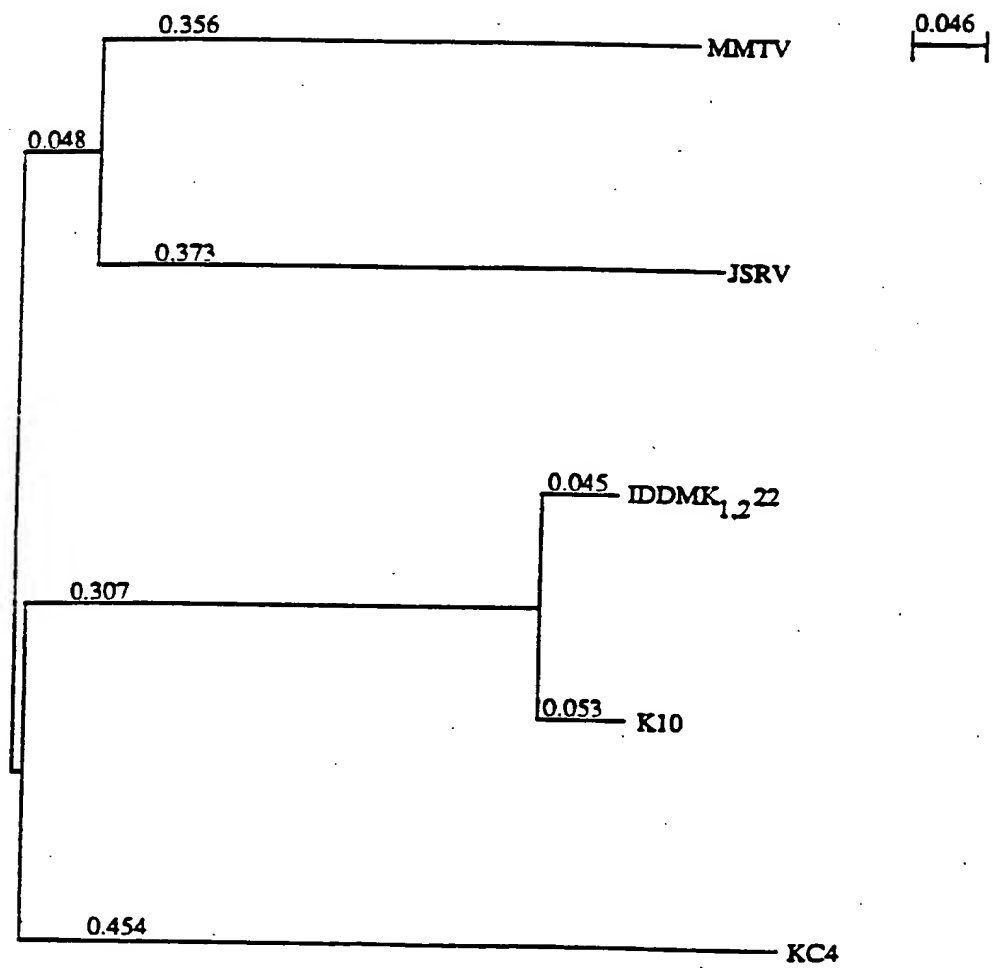
TEMPLATE	SPECIFICITY	IDDM PATIENTS (n=10)	CONTROLS (n=10)
RNA	RT+ U3-R		
	RT+ U3-R-POLY(A)		
	RT- U3-R		
	RT- U3-R-POLY(A)		
DNA			



FIGURE 3A.



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FIGURE 3B.

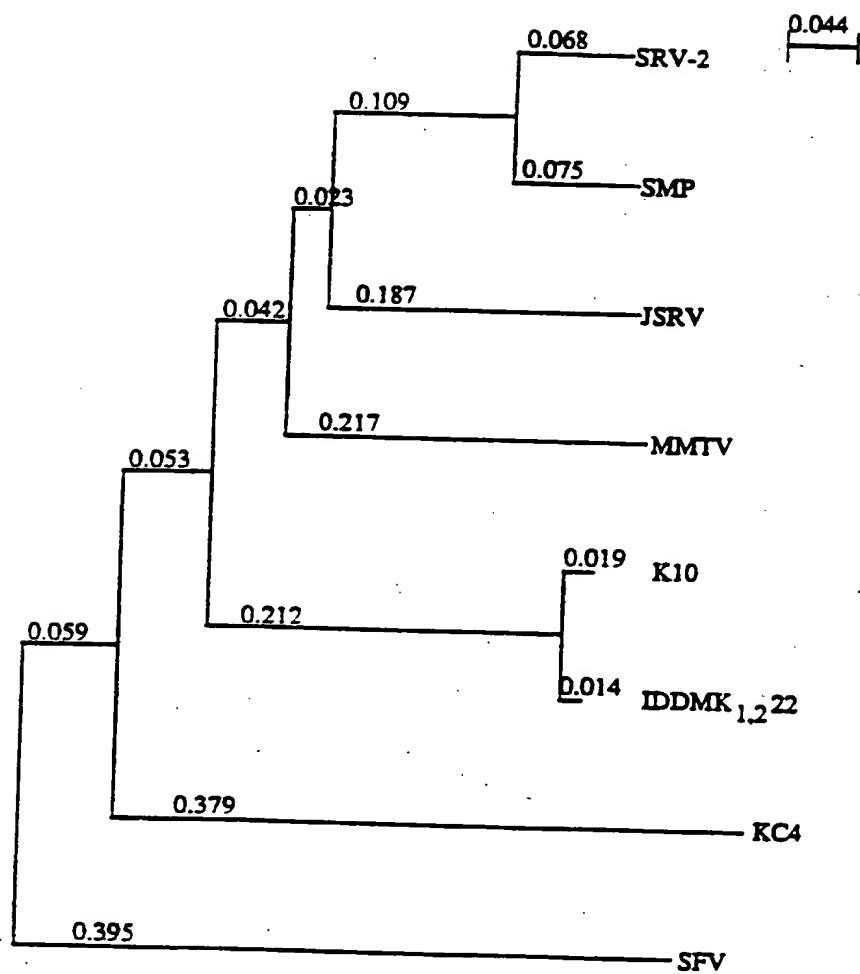


FIGURE 3C.

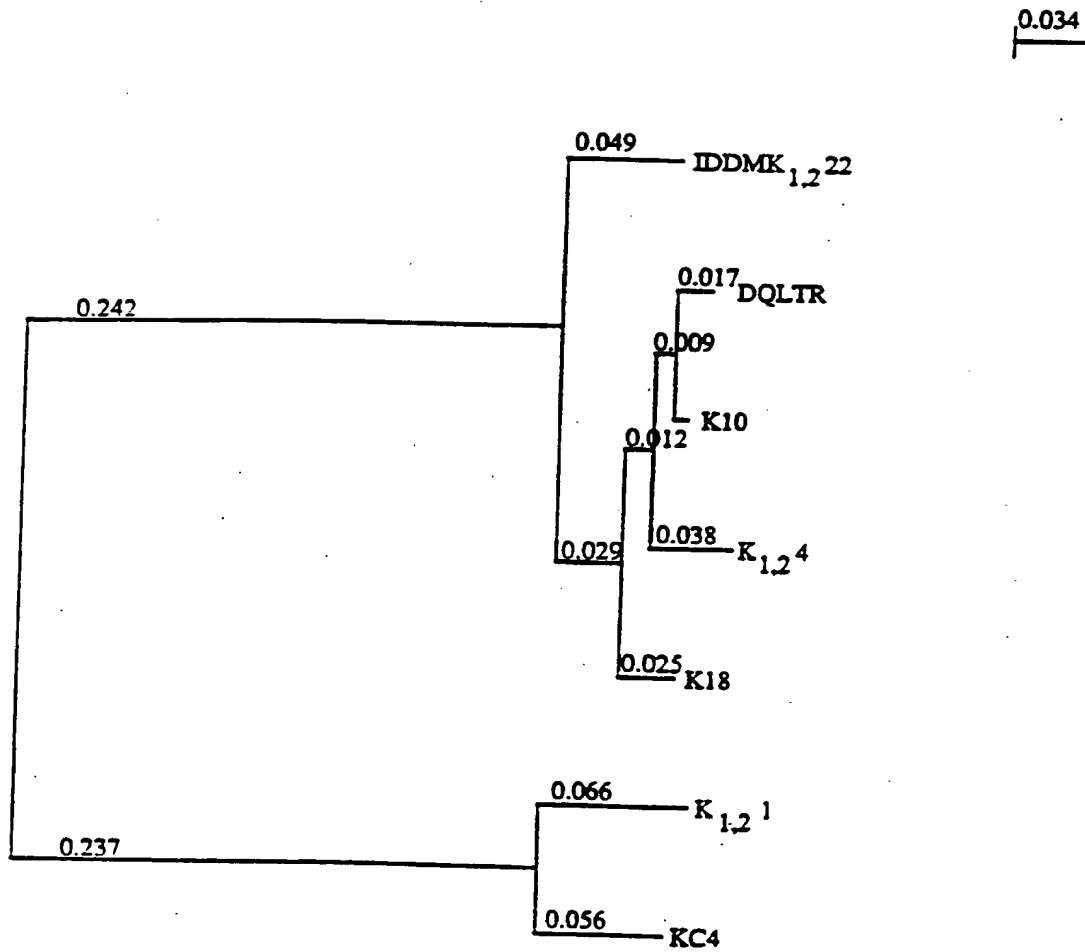


FIGURE 4A.

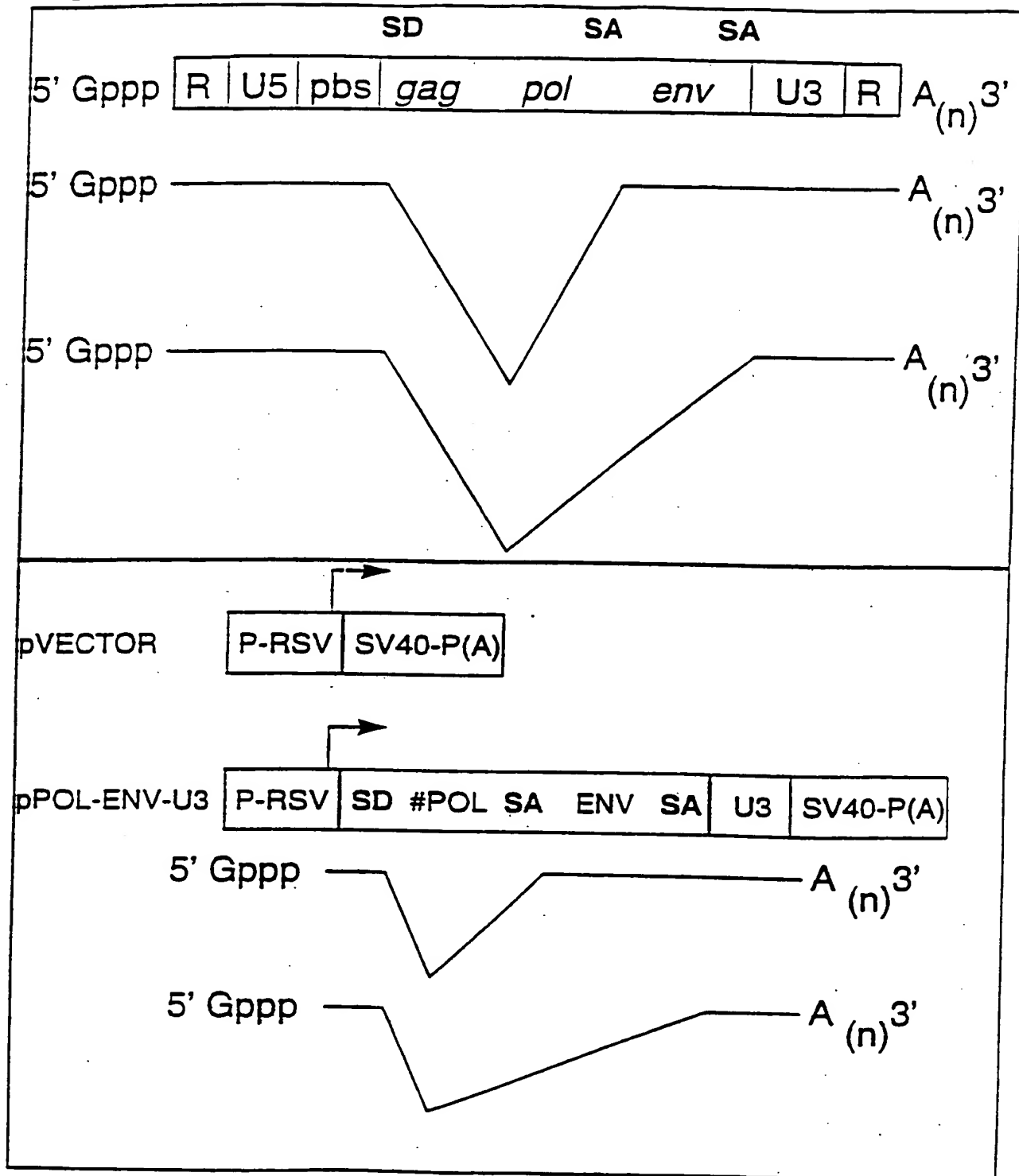


FIGURE 4B.

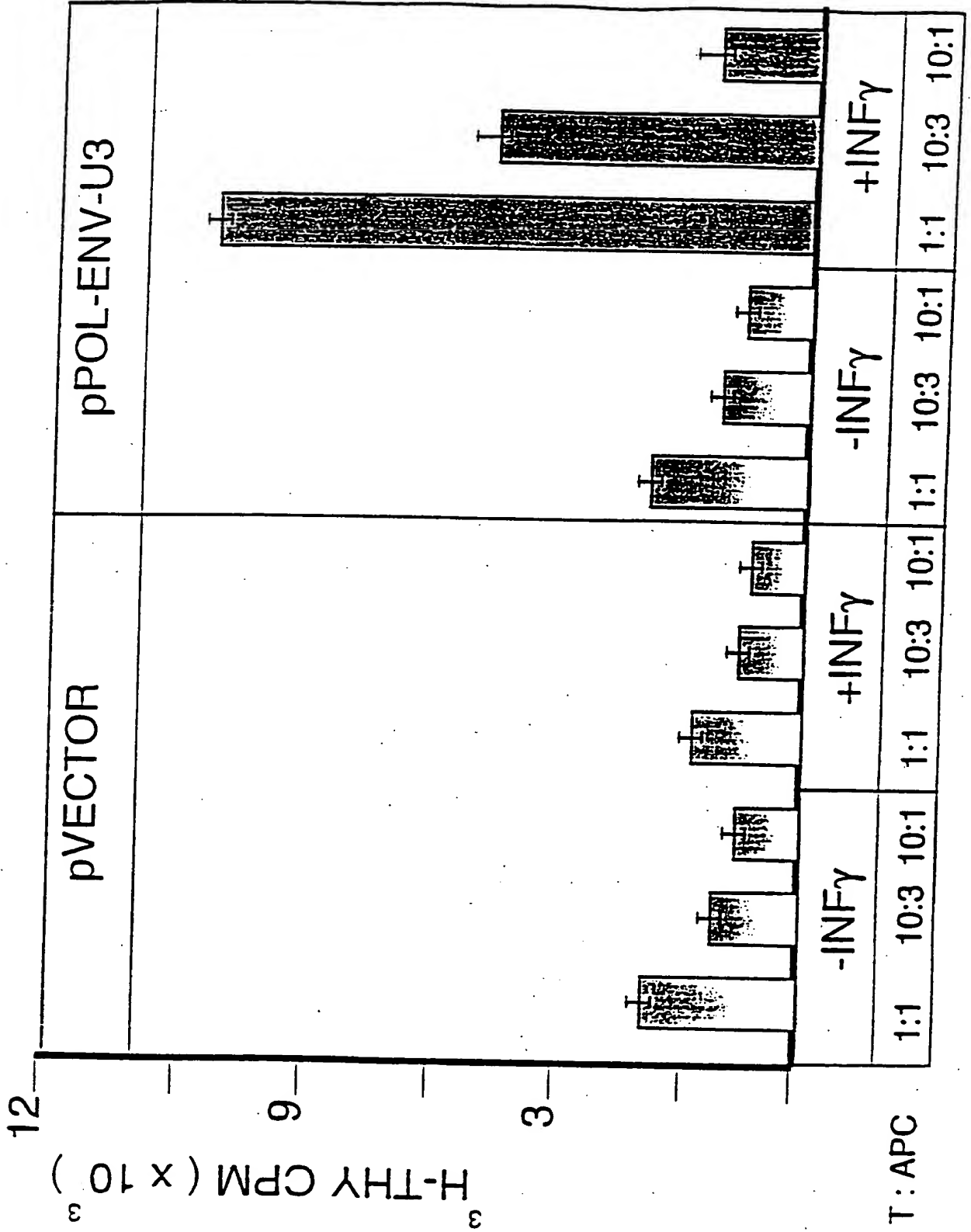
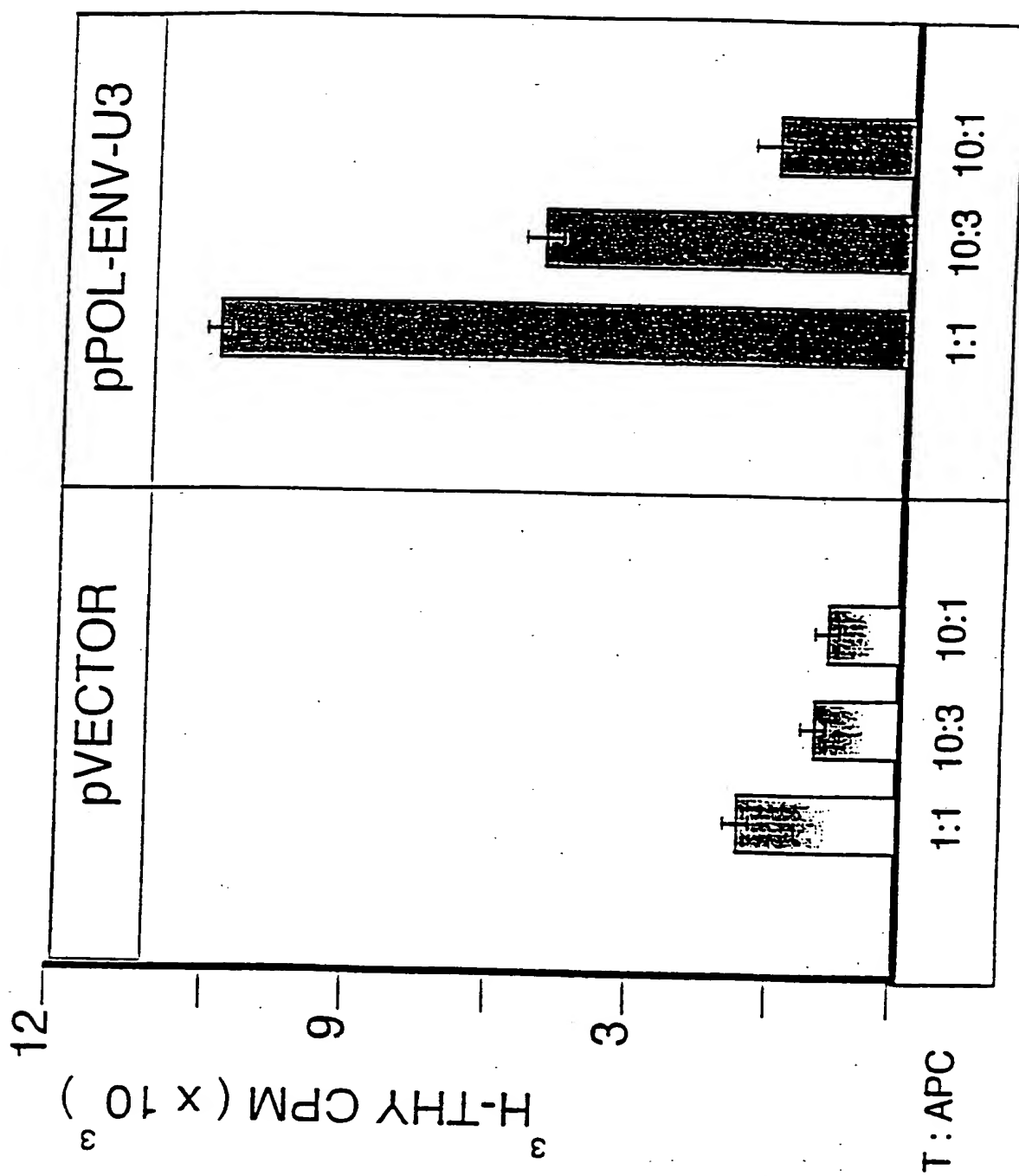


FIGURE 4C.



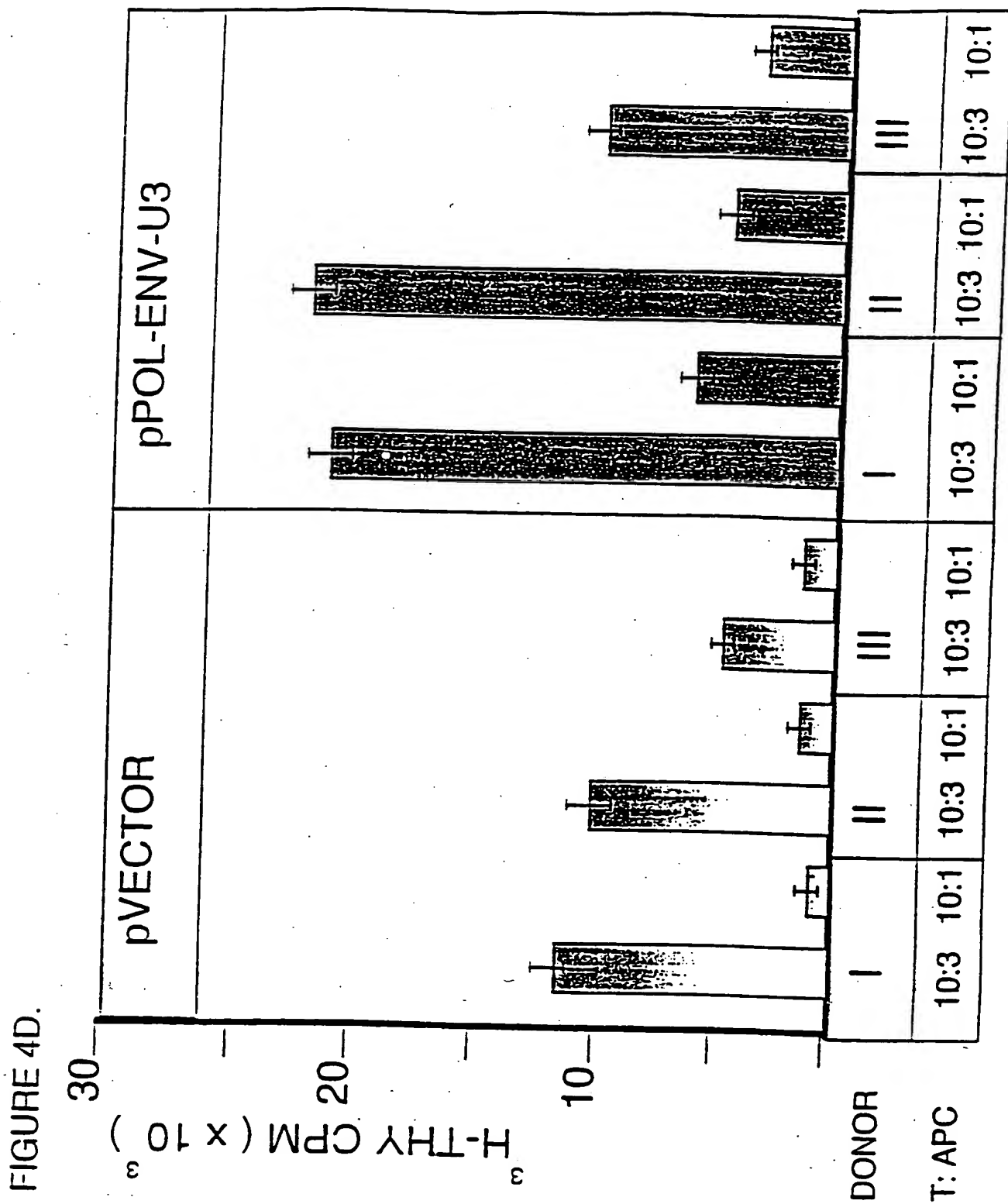


FIGURE 5.

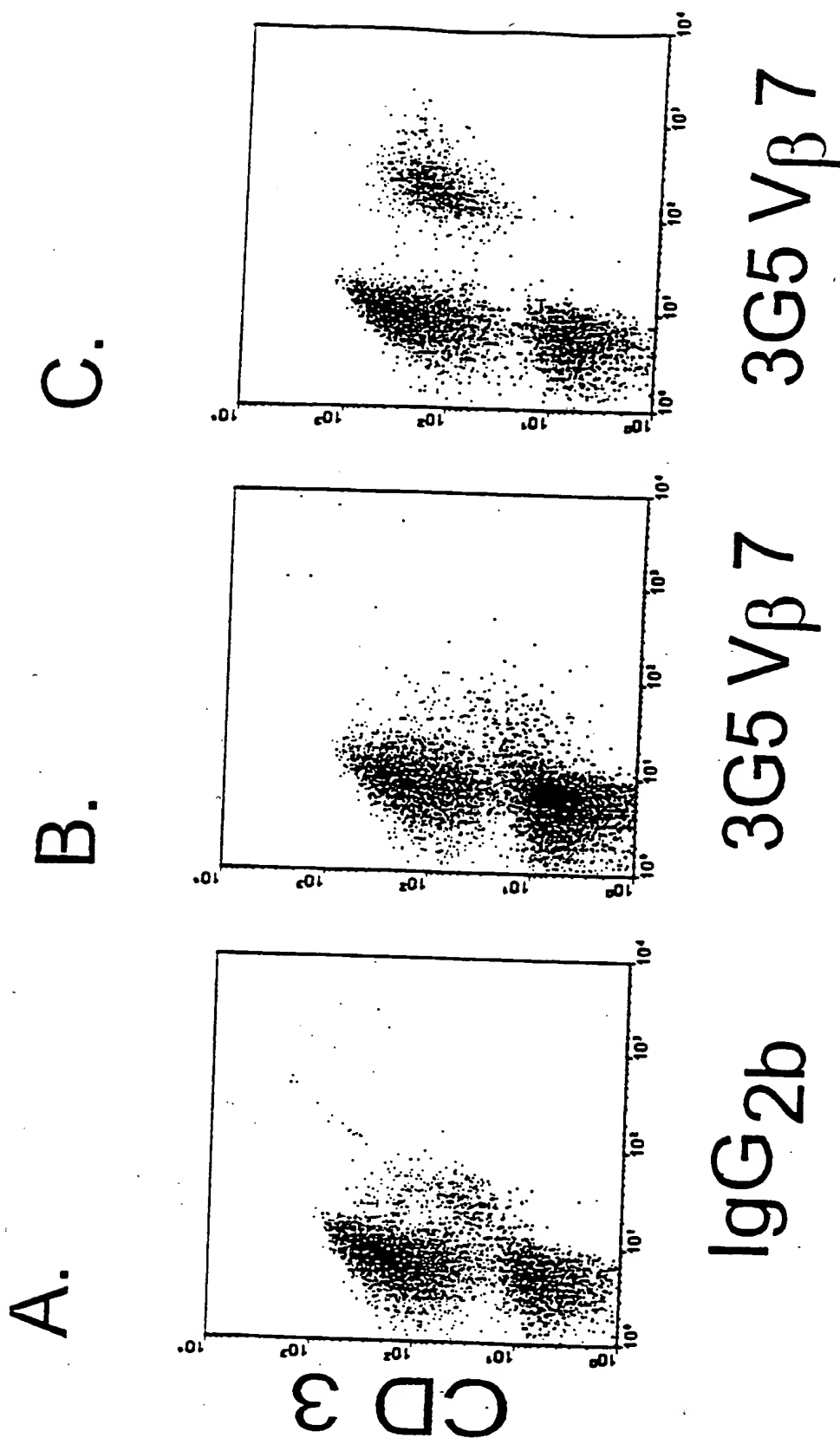
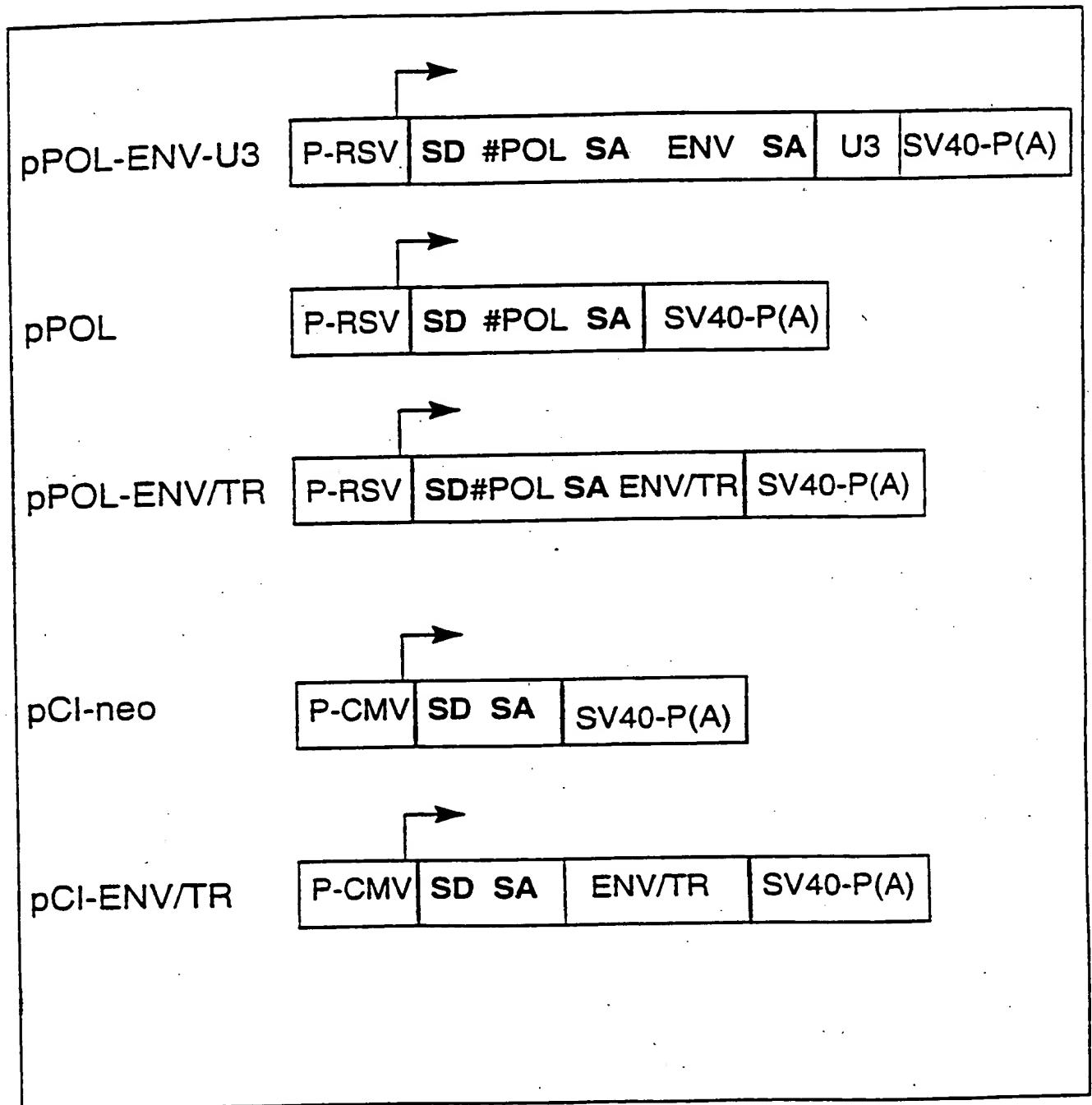


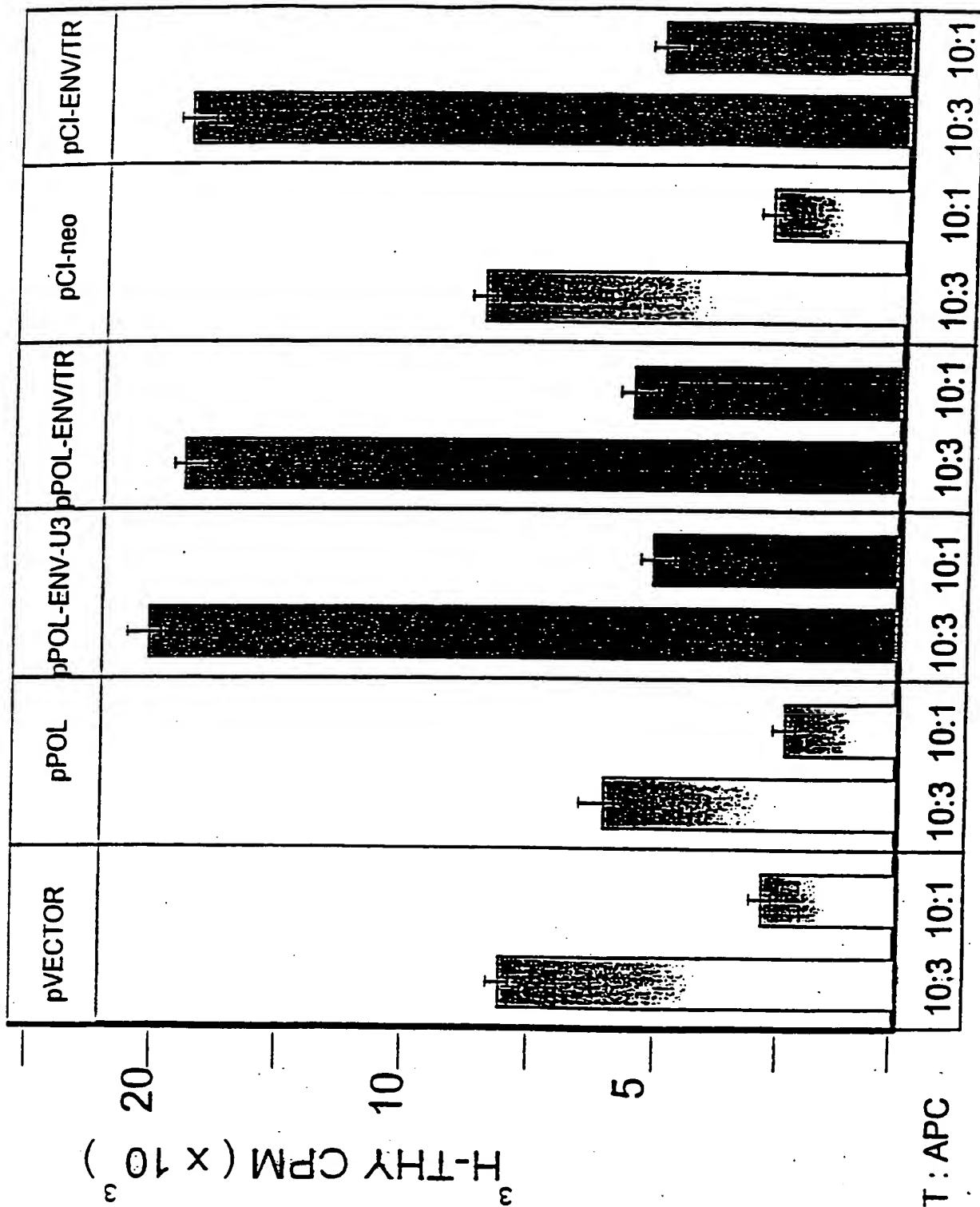


FIGURE 6A.



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FIGURE 6B.



## FIGURE 7A

iddmk1,2 22-5'1tr

CATCTCCCTCAGGAGAAACACCCACGAATGATCAATAAATACTAAGGGGACTCAGAGGCTGGT  
GGGATCCTCCATATGCTGAACGTTGGTTCCCGGGGCCCCCTTATTTCTTTCTCTATACTTTGT  
CTCTGTGTCTTTTTCTTTTCCAAGTCTTCTTCATTTGCACCTTACGAGAAACATCTCCATCAT  
GGTTGTTGGATGGGGGCAA

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FIGURE 7B

iddmk1,2 22-3'ltr

CTGCAGGTGTACCCAACAGCTCCGAAGAGACAGTGACATCGAGAACGGGGCCATGATGACGATG  
GCGGTTTTGTGCGAAAAGAAAAGGGGGAAATGTGGGGAAAAGCAAGAGAGATGAGATTGTTACT  
GTGTCTGTATAGAAAAGTAGACATAGGAGACTCCATTTTGTCTGTACTAAGAAAAATTCT  
TCTGCCCTTGAGATGCTGTTAATCTATGACCTTACCCCCAACCCCGTGCTCTCTGAAACATGTG  
CCGTGTCAAACTCAGGGTTAAATGGATTAAGGGTGGTGCAAGATGTGCTTTGTTAAACAGATG  
CTTGAAGGCAGCATGCTCATTAAGAGTCATCACCACTCCCTAATCTCAAGTACCCAGGGACAC  
AAACACTGCGAAAGGCCGCGAGGGACCTCTGCCTAGGAAAGCCAGGTATTGTCCAAGGTTTCTC  
CCCATGTGATAGTCTGAAATATGGCCTCGTGGGAAGGGAAAGACCTGACCATCCCCCAGACCA  
ACACCCGTAAAGGGTCTGTGCTGAGGAGGATTAGTATAAGAGGAAAGCATGCCTCTTGCAAGTT  
GAGAGAAGAGGAAGACATCTGTCTCCTGCCCATCCCCGTTGGGCAATGGAATGTCTCAGTATAAA  
ACCCGATTGAACATTCCATCTACTGAGATAGGGAAAAACTGCCTTAGGGCTGGAGGTGGGACA  
TGTGGGCAGCAATACTGCTTTGTAAAGCATTGAGATGTTTATGTGTATGTATATCTAAAAGCA  
CAGCACTTGATCCTTTACCTTGTCTATGATGCAAACACCTTTGTTACAGTGTTTGTCTGCTGA  
CCCTCTCCCCACTATTGTCTTGTGACCCTGACACATCTCCCTCAGGAGAAACACCCAcgaatg  
atcaataaataactaaggggactcagaggctggtgggatcctccatatgctgaacggttggttcc  
cggggcccccttatttctttctctatactttgtctctgtgtctttttctttttccaagtcttct  
tcatttgcaccttacgagaaacatctccatcatgggttggttgatgggggcaa

FIGURE 7C

iddmk1,2 22-env

ATGGTAACACCAGTCAATGGATGGATAATCCTATAGAAGTATATGTTAATGATAGTGTATGG  
GTACCTGGCCCCACAGATGATCGCTGCCCTGCCAAACCTGAGGAAGAAGGGATGATGATAAAT  
ATTTCCATTGGGTATCATTATCCTCCTATTTGCCTAGGGAGAGCACCAGGATGTTAATGCCT  
GCAGTCCAAAATTGGTTGGTAGAAGTACCTACTGTCACTCCTAACAGTAGATTCACTTATCAC  
ATGGTAAGCGGGATGTCACTCAGGCCACGGGTAAATTATTTACAAGACTTTTCTTATCAAAGA  
TCATTAAAATTTAGACCTAAAGGGAAAACCTGCCCAAGGAAATTCCTAAAGGATCAAAGAAT  
ACAGAAGTTTTAGTTTTGGGAAGAATGTGTGGCCAATAGTGTGGTGATATTACAAAACAATGAA  
TTCGGAATATTATAGATTAGGCACCTCGAGGTCAATTCTACCACAATTGCTCAGGACAAACT  
CAGTCGTGTCCAAGTGCAAGTGAGTCCAGCTGTGATAGCGACTTAACAGAAAGTCTAGAC  
AAACATAAGCATAAAAAATTACAGTCTTTCTACCTTTGGGAATGGGAAGAAAAAGGAATCTCT  
ACCCCAAGACCAAAAAATAAGTCTGTTTCTGGTCTGGAACATCCAGAATTGTGGAGGCTT  
AAGCCATTTTATACCTATCGACCTAAATTCCATTCTAACGGTTCCCTTACAAAGTTGCCTAAAG  
CCCCCTTATATGCTAGTTGTAGGAAATATAGTTATTAACCAGCCTCCCAAATATAACCTGT  
GAAAATTGTAGATTGTTTACTTGCATTGATTCAACTTTTAATTGGCAGCACCGTATTCTGCTG  
GTGAGAGCAAGAGAAGGCATGTGGATCCCTGTGTCCACGGACCGACCGTGGGAGGCCTCGCCA  
TCCATCCATATTTTGAAGTAAATATTAAGGCGTTTAAATAGATCCAAAAGATTCAATTTT  
ACTTTAATTGCAGTGATTATGGGATTAATTGCAGTCAAGCTACGGCTGCTGTGGCAGGGGTT  
GCATTGCACTCTTCTGTTCACTCAGTAAACTTTGTTAATTATTGGCAAAGAATTCTACAAGA  
TTGTGGAATTCACAATCTAGTATTGATCAAAAATTGGCAAGTCAAATTAATGATCTTAGACAA  
ACTGTCAATTTGGATGGGAGACAGGCTTGACTTAGAACATCATTTCCAGTTACAGTGTGACTGG  
AATACGTCAAGTTTTTGTATTACACCCCAAATTTATAATGAGTCTGAGCATCACTGGGACATG  
GTTAGACGCCATCTACAGGGAAGAGAAGATAATCTCACTTTAGACATTTCCAAATTAAGAA  
CAAATTTTCAAGCATCAAAGGCCATTTAAATTTGGTGCCAGGAACTGAGGCAATTGCAGGA  
GTTGCTGATGGCCTCGCAAATCTTAACCTGTCACTTGGATTAAGACCATCAGAAGTACTATG  
ATTATAAATCTCATATTAATCGTTGTGTGCCTGTTTTGTCTGTTGTTAGTCTGCAGGTGTACC  
CCAACAGCTCCGAAAAAAACAGTGACATCGAGAACGGGCCATGAATGACAAAGGCGGTTTTTG  
TTCAAAAAAAAAGGGGAAATTTTGGGGAAAACCAAAAAAATGAAAATGTT

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FIGURE 7D

ACA TTT GAA GTT CTA CAA TGA ACC CAT CAG AGA TGC AAA GAA AAG CGC CTC CAC GGA 57

GAT GGT AAC ACC AGT CAC ATG GAT GGA TAA TCC TAT AGA AGT ATA TGT TAA TGA TAG 114  
M V T P V T W M D N P I E V Y V N D S 19

TGT ATG GGT ACC TGG CCC CAC AGA TGA TCG CTG CCC TGC CAA ACC TGA GGA AGA AGG 171  
Y W V P G P T D D R C P A K P E E E G 38

GAT GAT GAT AAA TAT TTC CAT TGG GTA TCA TTA TCC TCC TAT TTG CCT AGG GAG AGC 228  
M M I N I S I G Y H Y P P I C L G R A 57

ACC AGG ATG TTT AAT GCC TGC AGT CCA AAA TTG GTT GGT AGA AGT ACC TAC TGT CAG 285  
P G C L M P A V Q N W L V E V P T V S 76

TCC TAA CAG TAG ATT CAC TTA TCA CAT GGT AAG CGG GAT GTC ACT CAG GCC ACG GGT 342  
P N S R F T Y H M V S G M S L R P R V 95

AAA TTA TTT ACA AGA CTT TTC TTA TCA AAG ATC ATT AAA ATT TAG ACC TAA AGG GAA 399  
N Y L Q D F S Y Q R S L K F R P K G K 114

AAC TTG CCC CAA GGA AAT TCC TAA AGG ATC AAA GAA TAC AGA AGT TTT AGT TTG GGA 456  
T C P K E I P K G S K N T E V L V W E 133

AGA ATG TGT GGC CAA TAG TGT GGT GAT ATT ACA AAA CAA TGA ATT CGG AAC TAT TAT 513  
E C V A N S V V I L Q N N E F G T I I 152

AGA TTA G 520  
D 153

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## FIGURE 7E

k1,2-22-env/fs

ACATTTGAAGTTCTACAATGAACCCATCAGAGATGCAAAGAAAAGCGCCTCCACGGAGATGGTA  
ACACCAAGTCACATGGATGGATAATCCTATAGAAGTATATGTTAATGATAGTGTATGGGTACCTG  
GCCCCACAGATGATCGCTGCCCTGCCAAACCTGAGGAAGAAGGGATGATGATAAATATTTCCAT  
TGGGTATCATTATCCTCCTATTTGCCTAGGGAGAGCACCAGGATGTTTAATGCCTGCAGTCCAA  
AATTGGTTGGTAGAAGTACCTACTGTCAGTCCTAACAGTAGATTCACTTATCACATGGTAAGCG  
GGATGTCACTCAGGCCACGGGTAAATTATTTACAAGACTTTTCTTATCAAAGATCATTAAAATT  
TAGACCTAAAGGGAAAACCTTGCCCCAAGGAAATTCCTAAAGGATCAAAGAATACAGAAGTTTTA  
GTTTGGGAAGAATGTGTGGCCAATAGTGTGGTGATATTACAAAACAATGAATTCGGAACCTATTA  
TAGATTAGGCACCTCGAGGTCAATTCTACCACAATTGCTCAGGACAAACTCAGTCGTGTCCAAG  
TGCACAAGTGAGTCCAGCTGTGCGATAG

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## FIGURE 7F

iddmk1,2 22-ENV

MVTPVTWMDNPIEVYVND SVWVPGPTDDRCPAKPEEEGMMINISIGYHYPPICLGRA  
PGCLMPAVQNWLV E VPTVSPNSRFTYH MVSGMSLRPRVNYLQDFS YQRSLKFRPKG  
KTC PK EIPK GSKNTEVLVWEECVANSV VILQNN EFGTIDZAPRGQFYHNC SGQTQSC  
PSAQVSPA VDSDLTESLDKHKHKKLQSFYLWEWEEKGISTPRPKIISPVS GP EHP EL  
WRLTVASHHIRIW SGNQTL ETRYRKPFYTIDLNSILTVPLQ SCLKPPYMLVVGNTVIKP  
ASQTITCENCRLFTCIDSTFNWQHRILLVRAREGMWIPVSTDRPWEASPSIHILTEILK  
GVLNRSKR FIFTLIAVIMGLIAVTATAAVAGVALHSSVQSVNFVNYWQKNSTR LWNS  
QSSIDQKLASQINDLRQTVIWMGDRLDLEHHFQLQCDWNTSDFCITPQIYNESEHH  
WDMVRRHLQGREDNLTLDISKLKEQIFEASKAHLNLVPGTEA IAGVADGLANLNPVT  
WIKTIRSTMIINLILIVCLFCLLLVCRCTPTAPKKT VTSRTGHE

004210"00205450



FIGURE 7G

ACATTTGAAGTTCTACAATGAACCCATCAGAGATGCAAAGAAAAGCGCCTCCACGGAGATGCT 63  
 AACACCAAGTCACATGGATGGATAATCCTATAGAAGTATATGTTAATGATAGTGTATGGGTACC 2  
 T P V T W M D N P I E V Y V N D S V W V P M V 126  
 TGGCCCCACAGATGATCGCTGCCCTGCCAAACCTGAGGAAGAAGGGATGATGATAAATATTTC 23  
 G P T D D R C P A K P E E E G M M I N I S 189  
 CATTGGGSTATCATTATCCTCCTATTTGCCTAGGGAGAGCACCAGGATGTTTAATGCCTGCAGT 44  
 I G Y H Y P P I C L G R A P G C L M P A V 252  
 CCAAATTTGGTTGGTAGAAGTACCTACTGTCTAGTCCTAACAGTAGATTCACTTATCACATGCT 65  
 Q N W L V E V P T V S P N S R F T Y H M V 315  
 AAGCGGGATGTCACTCAGGCCACGGGTAAATTATTACAGACTTTTCTTATCAAAGATCATT 86  
 S G M S L R P R V N Y L Q D F S Y Q R S L 378  
 AAAATTTAGACCTAAAGGGAAAACCTGCCCAAGGAAATTCCTAAAGGATCAAAGAATACAGA 107  
 K F R P K G K T C P K E I P K G S K N T E 431  
 AGTTTGTAGTTTCGGAAGAATGTGTGGCCAATAGTGTGGTGATATTACAAAACAATGAATTCGG 128  
 V L V W E E C V A N S V V I L O N N E F G 504  
 AACTATTATAGATTTAGGCACCTCGAGGTCAATTCTACCACAATTGCTCAGGACAAACTCAGT 149  
 T I I D L G T S R S I L P O L L R T N S V 567  
 CGTGTCCAAGTGCACAAGTGAGTCCAGCTGTCTGATAG 170  
 V S K C T S E S S C R 601  
 181

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 0044270 00205459

## FIGURE 7H

iddmk1,2 22-POL

FTIPLAEQDCEKFAFTIPAINNKEPATRFQWKVLPQGMLNSPTICQTFVGRALQPVRDKFSDC  
YIIHYFDDILCAAETKDKLIDCYTFLPAEVANAGLAIASDKIQTSTPFHYLGMQIENRRKIKPQ  
KIEIRKDTLKTLDNFQKLLGDINWIRPTLGIPTYAMSNLFSILRGDSDLNSKRMLT

004270 030545Z

**FIGURE 8A****k1,2-1**

gtaaatgacacctatgatgcactgccaccctttcactgtttcaccctgaacatctgctttttac  
atctaagtgattgtacccaataaatagtgtggagaccagagctctgagccttttgagcctcca  
ttttgcaactggteccctggctcccacctttatgaactcttaacctgtcttttctcattccttt  
gtcaccattggactttgggtaccctacgggtggtgttgaggctgtcaccgcacattaa

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## FIGURE 8B

k1,2-10

gttagttaatctataatctatagagacaatgcttatcactggcttgctgtcaataaatatgtg  
ggtaaatctctgttcaagactctcagctttgaagctgtgagaccctgatttcccactccacac  
ctctatatttctgtgtgtgtgtctttaattcctccagtgttgctgggttaggggtctcctcgacg  
agctgtcgtgc

004370.004660

## FIGURE 8C

x1,2-16

aactcagctgctgcacagtgggtcgagcctccagagctcatgccattgcagtgggtcagagcctg  
gccctcctcttcctgcatagaacctggattcaatctgtaaggtgggaagtgcagcagcagaga  
actctggccttgagagagtcctctgttcccacttcactttccttttcaccaaataaaaccctg  
ctttcactcatgcatcaaattgtctgtgagcctacatTTTTgtggccatgggacaagaacacc  
atctttagctgagctagggaaaagtcctgca

004370 004370 004370

## FIGURE 8D

x1,2-17

gatgtgaccactgtgacctacctacactggagatggctcacacttccttacccttcccctgct  
gtaccaataaataacagcacagcctgacattcggagccattacoggtctttgtgacttgggtgg  
tagtggtatcccctagggcccagctgtcttttcttttatctctttgtcttgtgtctttatttc  
tatgagtctctcgtctccgcacatggggagaaaaacccatagaccctgtagggctg

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**FIGURE 8E****x1,2-26**

ctcacaaaaataataaaaagcttctgttggccattcttcagatcttcattctcttgaggatcc  
ccctgtacatgtaaaaatgtaataaaacttgtatcctttctcctcttaattctgtcttgcatca  
atatcattcctagaccagtcagagatgggtggagggtgagccgtacatttccta

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## FIGURE 8F

k1,2-27

cagagaactccagccagctgtgatggagcctcaggaagttcacagttgcagcaggaaggagcctggc  
tgctcctcttcctgtgtggaacctgggattagaacaggctggcaggaagtgttttagcagggactct  
ggcctactcacactccttgtttccccctttcttccttttcaactcaataaagccctgtcttactcac  
cattcaaattgtctgtgagcctgaattttcatggctgtgggacaaagaaccctatttttagctgaac  
taaggaaaattcctgcaaa

004210" 00206450



## FIGURE 8G

k1,2-4

gtgattgtctgctgaccctctccccacaattgtcttgtagaccctgacacatccccctcttcga  
gaaacacccgcggatgatcaataaataattaaggggaactcagaggctggcaggatcctccatat  
gctgaacgctgggtgccccgggtcccccttctttctttctctataactttgtctctgtgtctttt  
tcttttccaaatctctcgtcccaccttacgagaaacacccacaggtgtgtccgggcaacccaa  
cgccacataaca

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FIGURE 9

